

# Blast 2 Sequences results

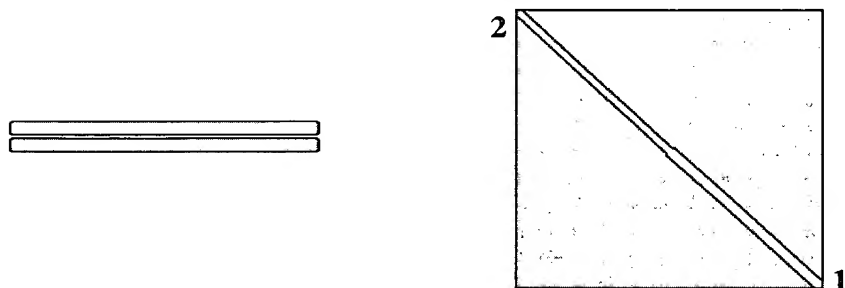
[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match:  Mismatch:  gap open:  gap extension: x\_dropoff:  expect:  wordsize:  ☐ Filter 

Sequence 1 lcl|60/054,212 SIN:4 Length 955 (1 .. 955)

Sequence 2 lcl|09/820,649 SIN:12 Length 955 (1 .. 955)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1836 bits (955), Expect = 0.0

Identities = 955/955 (100%)

Strand = Plus / Minus

```
Query: 1   tcgagtttttttttttttttttttgtttttatggcatttgtttctttattgaaaatatttg 60
          |||
Sbjct: 955 tcgagtttttttttttttttttttgtttttatggcatttgtttctttattgaaaatatttg 896
```

```
Query: 61   tcttcttgccattagaacacaagcattgtggatggcagagacttgactgttcacatctgta 120
          |||
Sbjct: 895   tcttcttgccattagaacacaagcattgtggatggcagagacttgactgttcacatctgta 836
```

```
Query: 121  tctgctggaataacttattaaatggatgagtaactccttaggccagtgtcagcattgctgt 180
          |||
Sbjct: 835   tctgctggaataacttattaaatggatgagtaactccttaggccagtgtcagcattgctgt 776
```

```
Query: 181  catcccaggacctacctttgggtcccatacaagtagaagaagtcacagtagaagatggttt 240
          |||
Sbjct: 775   catcccaggacctacctttgggtcccatacaagtagaagaagtcacagtagaagatggttt 716
```

```
Query: 241  gtactactccagacacgactgcaatttggtcatagaaattctcagtctggtaccgcctga 300
          |||
Sbjct: 715   gtactactccagacacgactgcaatttggtcatagaaattctcagtctggtaccgcctga 656
```

```
Query: 301  tccagttagccaggtagagtgtcccgtacagacccagaaagaacaggtagtgtgtagttag 360
          |||
Sbjct: 655   tccagttagccaggtagagtgtcccgtacagacccagaaagaacaggtagtgtgtagttag 596
```

Query: 361 tgggtctcagcctctccagtccttgctgatcatgaagagctggggcaggatagccactgatt 420  
 |||||  
 Sbjct: 595 tgggtctcagcctctccagtccttgctgatcatgaagagctggggcaggatagccactgatt 536

Query: 421 ccagatagatagagaaagtccagaggatctccagcagagtgaactgtagttttcaagga 480  
 |||||  
 Sbjct: 535 ccagatagatagagaaagtccagaggatctccagcagagtgaactgtagttttcaagga 476

Query: 481 aggaaaggccaatgactgggaccagaagaaactccaggcggaatgtgtcattctcactgt 540  
 |||||  
 Sbjct: 475 aggaaaggccaatgactgggaccagaagaaactccaggcggaatgtgtcattctcactgt 416

Query: 541 caaaagtttttacggaatttcccatatatcatgtacactgtaacataggcacagaggagaa 600  
 |||||  
 Sbjct: 415 caaaagtttttacggaatttcccatatatcatgtacactgtaacataggcacagaggagaa 356

Query: 601 aaaccaccttcattactgtgtttagatggagatgaagttggtgaacaggtccaggtacc 660  
 |||||  
 Sbjct: 355 aaaccaccttcattactgtgtttagatggagatgaagttggtgaacaggtccaggtacc 296

Query: 661 tgggtggtgaagacgagagcaaacaggatctggctcttcccagagatgcccttgcagcact 720  
 |||||  
 Sbjct: 295 tgggtggtgaagacgagagcaaacaggatctggctcttcccagagatgcccttgcagcact 236

Query: 721 tggacctccagatcttccccagcagcaagatcatggccaggaggtggctcaggtcgccga 780  
 |||||  
 Sbjct: 235 tggacctccagatcttccccagcagcaagatcatggccaggaggtggctcaggtcgccga 176

Query: 781 ggattcggaacacggttcattggtccagccagtcagtcgtgcgccccgcgccagcaaacttc 840  
 |||||  
 Sbjct: 175 ggattcggaacacggttcattggtccagccagtcagtcgtgcgccccgcgccagcaaacttc 116

Query: 841 taggaaaactttctggcgggcagggcggtgccacgtctccggccccggtctctaggtgcc 900  
 |||||  
 Sbjct: 115 taggaaaactttctggcgggcagggcggtgccacgtctccggccccggtctctaggtgcc 56

Query: 901 ccagagccctgcctgcgcttcacagctccgcgatcgacccgcgcgcgcgcgcgc 955  
 |||||  
 Sbjct: 55 ccagagccctgcctgcgcttcacagctccgcgatcgacccgcgcgcgcgcgcgc 1

CPU time: 0.01 user secs. 0.01 sys. secs 0.02 total secs.

Lambda K H  
 1.33 0.621 1.12

Gapped  
 Lambda K H  
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 16  
 Number of Sequences: 0  
 Number of extensions: 16  
 Number of successful extensions: 15  
 Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 955  
length of database: 10,130,642,339  
effective HSP length: 25  
effective length of query: 930  
effective length of database: 10,130,642,314  
effective search space: 9421497352020  
effective search space used: 9421497352020  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 21 (41.1 bits)